

1223

#20



OIKE

RAW SEQUENCE LISTING

DATE: 01/06/2003

PATENT APPLICATION: US/09/584,411C

TIME: 13:51:53

Input Set : A:\CURA52.APP.txt

Output Set: N:\CRF4\01062003\I584411C.raw

5 <110> APPLICANT: Shimkets, Richard
6 Fernandes, Elma
7 Hermann, John
8 Vernet, Corine
10 <120> TITLE OF INVENTION: Novel Polynucleotides and Polypeptides Encoded Thereby
12 <130> FILE REFERENCE: 15966-552
14 <140> CURRENT APPLICATION NUMBER: 09/584,411C
15 <141> CURRENT FILING DATE: 2000-05-31
17 <150> PRIOR APPLICATION NUMBER: USSN 60/137,322
18 <151> PRIOR FILING DATE: 1999-06-03
20 <150> PRIOR APPLICATION NUMBER: USSN 60/189,810
21 <151> PRIOR FILING DATE: 2000-03-16
23 <150> PRIOR APPLICATION NUMBER: USSN 60/191,158
24 <151> PRIOR FILING DATE: 2000-03-22
26 <150> PRIOR APPLICATION NUMBER: USSN 60/193,086
27 <151> PRIOR FILING DATE: 2000-03-30
29 <150> PRIOR APPLICATION NUMBER: USSN 60/201,388
30 <151> PRIOR FILING DATE: 2000-05-03
32 <160> NUMBER OF SEQ ID NOS: 93
34 <170> SOFTWARE: PatentIn Ver. 2.0
36 <210> SEQ ID NO: 1
37 <211> LENGTH: 836
38 <212> TYPE: DNA
39 <213> ORGANISM: Artificial Sequence
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43 <222> LOCATION: (189)..(695)
46 <220> FEATURE:
47 <223> OTHER INFORMATION: Description of Artificial Sequence: chemically
49 synthesized
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56 gcggccgcca cctggagttt cttcagactc cagatttccc tgtcaaccac gaggagtcca 120
60 gagaggaaac gcggagcgga gacaacagta cctgacgcct ctttcagccc gggatcgccc 180
64 cagcaggg atg ggc gac aag atc tgg ctg ccc ttc ccc gtg ctc ctt ctg 230
66 Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu
68 1 5 10
72 gcc gct ctg ctt cgg gtg ctg ctg cct ggg gcg gcc ggc ttc aca cct 278
74 Ala Ala Leu Leu Arg Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro
76 15 20 25 30
80 tcc ctc gat agc gac ttc acc ttt acc ctt ccc gcc ggc cag aag gag 326
82 Ser Leu Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu
84 35 40 45

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90 Cys Phe Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr
92          50          55          60
96 caa gtt tta gat gga gca gga tta gat att gat ttc cat ctt acc tct 422
98 Gln Val Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Thr Ser
100        65          70          75
104 cca gaa ggc aaa acc tta gtt ttt gaa caa aga aaa tca gat gga gtt 470
106 Pro Glu Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val
108        80          85          90
112 cac act gta gag act gaa gtt ggt gat tac atg ttc tgc ttt gac aat 518
114 His Thr Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn
116 95          100          105          110
120 aca ttc agc acc att tct gag aag gtg att ttc ttt gaa tta atc ctg 566
122 Thr Phe Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu
124          115          120          125
128 gat aat atg gga gaa cag gca caa gaa caa gaa gat tgg aag aaa tat 614
130 Asp Asn Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr
132          130          135          140
136 att act ggc aca gat ata ttg gat atg aaa ctg gaa gac atc ctg gac 662
138 Ile Thr Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Asp
140          145          150          155
144 ctg ccc ggg cgg ccg ctc gag ccc tat agt gag taagtctgga ggcccgggcg 715
146 Leu Pro Gly Arg Pro Leu Glu Pro Tyr Ser Glu
148        160          165
152 gccgctcctg cagtagggta ccgagctcgt cgacgcatgc tgatctagat cttaattaac 775
156 acgtggtgcc aagctttgga agactcagct tttgttcctt ttagtgaggg ttaatttcga 835
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169 <223> OTHER INFORMATION: Description of Artificial Sequence: chemically
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179 Leu Leu Arg Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
181        20          25          30
185 Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
187        35          40          45
191 Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
193        50          55          60
197 Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Thr Ser Pro Glu
199 65          70          75          80
203 Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
205          85          90          95
209 Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe
211        100          105          110

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215 Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn
217      115      120      125
221 Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr
223      130      135      140
227 Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Asp Leu Pro
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235      165
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289                                     Met Ser Trp
291                                     1
295 ggc acg gag ctg tgg gat cag ttc gac agc tta gac aag cat aca caa 166

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297 Gly Thr Glu Leu Trp Asp Gln Phe Asp Ser Leu Asp Lys His Thr Gln
299      5      10      15
303 tgg gga att gac ttc ttg gaa aga tat gcc aaa ttt gtt aaa gag agg 214
305 Trp Gly Ile Asp Phe Leu Glu Arg Tyr Ala Lys Phe Val Lys Glu Arg
307 20      25      30      35
311 ata gaa att gaa cag aac tat gcg aaa caa ttg aga aat ctg gtt aag 262
313 Ile Glu Ile Glu Gln Asn Tyr Ala Lys Gln Leu Arg Asn Leu Val Lys
315      40      45      50
319 aag tac tgc ccc aaa cgt tca tcc aaa gat gaa gag cca cgg ttt acc 310
321 Lys Tyr Cys Pro Lys Arg Ser Ser Lys Asp Glu Glu Pro Arg Phe Thr
323      55      60      65
327 tcg tgt gta gcc ttt ttt aat atc ctt aat gag tta aat gac tat gca 358
329 Ser Cys Val Ala Phe Phe Asn Ile Leu Asn Glu Leu Asn Asp Tyr Ala
331      70      75      80
335 gga cag cga gaa gtt gta gca gaa gaa atg gcg cac aga gtg tat ggt 406
337 Gly Gln Arg Glu Val Val Ala Glu Glu Met Ala His Arg Val Tyr Gly
339      85      90      95
343 gaa tta atg aga cat gct cat gat ctg aaa act gaa aga aaa atg cat 454
345 Glu Leu Met Arg His Ala His Asp Leu Lys Thr Glu Arg Lys Met His
347 100      105      110      115
351 ctg caa gaa ggc cga aaa gct cac caa tct ctt gcc atg tgc tgg aac 502
353 Leu Gln Glu Gly Arg Lys Ala His Gln Ser Leu Ala Met Cys Trp Asn
355      120      125      130
359 cag atg gat aat agt aaa aag aag ttt gaa aga gaa tgt aga gag gca 550
361 Gln Met Asp Asn Ser Lys Lys Lys Phe Glu Arg Glu Cys Arg Glu Ala
363      135      140      145
367 gaa aag gcc cac cag agt tat gaa aga ttg gat aat gat act aat gca 598
369 Glu Lys Ala His Gln Ser Tyr Glu Arg Leu Asp Asn Asp Thr Asn Ala
371      150      155      160
375 acc aag gca gat gtt gaa aat gcc aaa cag cag ttg aat ctg cgt acg 646
377 Thr Lys Ala Asp Val Glu Asn Ala Lys Gln Gln Leu Asn Leu Arg Thr
379      165      170      175
383 cat atg gcc gat gaa aat aaa aat gca tat gct gca caa tta caa aac 694
385 His Met Ala Asp Glu Asn Lys Asn Ala Tyr Ala Ala Gln Leu Gln Asn
387 180      185      190      195
391 ttt aat gga gaa caa cat aaa cat ttt tat gta gtg att cct cag att 742
393 Phe Asn Gly Glu Gln His Lys His Phe Tyr Val Val Ile Pro Gln Ile
395      200      205      210
399 tac aag caa cta caa gaa atg gac gaa cga agg act att aaa ctc agt 790
401 Tyr Lys Gln Leu Gln Glu Met Asp Glu Arg Arg Thr Ile Lys Leu Ser
403      215      220      225
407 gag tgt tac aga gga ttt gct gac tca gaa cgc aaa gtt att ccc atc 838
409 Glu Cys Tyr Arg Gly Phe Ala Asp Ser Glu Arg Lys Val Ile Pro Ile
411      230      235      240
415 att tca aaa tgt ttg gaa gga atg att ctt gca gca aaa tca gtt gat 886
417 Ile Ser Lys Cys Leu Glu Gly Met Ile Leu Ala Ala Lys Ser Val Asp
419      245      250      255
423 gaa aga aga gac tct caa atg gtg gta gac tcc ttc aaa tct ggt ttt 934
425 Glu Arg Arg Asp Ser Gln Met Val Val Asp Ser Phe Lys Ser Gly Phe

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427	260					265				270				275			
431	gaa	cct	cca	gga	gac	ttt	cca	ttt	gaa	gat	tac	agt	caa	cat	ata	tat	982
433	Glu	Pro	Pro	Gly	Asp	Phe	Pro	Phe	Glu	Asp	Tyr	Ser	Gln	His	Ile	Tyr	
435					280					285				290			
439	aga	acc	att	tct	gat	ggg	act	atc	agt	gca	tcc	aaa	cag	gag	agt	ggg	1030
441	Arg	Thr	Ile	Ser	Asp	Gly	Thr	Ile	Ser	Ala	Ser	Lys	Gln	Glu	Ser	Gly	
443				295					300					305			
447	aag	atg	gat	gcc	aaa	acc	cca	gta	gga	aag	gcc	aag	ggc	aaa	ttg	tgg	1078
449	Lys	Met	Asp	Ala	Lys	Thr	Pro	Val	Gly	Lys	Ala	Lys	Gly	Lys	Leu	Trp	
451			310					315						320			
455	ctc	ttt	gga	aag	aag	cca	aag	ggc	cca	gca	cta	gaa	gat	ttc	agt	cat	1126
457	Leu	Phe	Gly	Lys	Lys	Pro	Lys	Gly	Pro	Ala	Leu	Glu	Asp	Phe	Ser	His	
459		325				330						335					
463	ctg	cca	cca	gaa	cag	aga	cgt	aaa	aaa	cta	cag	cag	cgc	att	gat	gaa	1174
465	Leu	Pro	Pro	Glu	Gln	Arg	Arg	Lys	Lys	Leu	Gln	Gln	Arg	Ile	Asp	Glu	
467	340					345				350						355	
471	ctt	aac	aga	gaa	cta	cag	aaa	gaa	tca	gac	caa	aaa	gat	gca	ctc	aac	1222
473	Leu	Asn	Arg	Glu	Leu	Gln	Lys	Glu	Ser	Asp	Gln	Lys	Asp	Ala	Leu	Asn	
475				360						365						370	
479	aaa	atg	aaa	gat	gta	tat	gag	aag	gat	cca	caa	atg	ggg	gat	cca	ggg	1270
481	Lys	Met	Lys	Asp	Val	Tyr	Glu	Lys	Asp	Pro	Gln	Met	Gly	Asp	Pro	Gly	
483				375						380						385	
487	agt	ttg	cag	cct	aaa	tta	gca	gag	acc	atg	aat	aac	att	gac	cgc	cta	1318
489	Ser	Leu	Gln	Pro	Lys	Leu	Ala	Glu	Thr	Met	Asn	Asn	Ile	Asp	Arg	Leu	
491			390					395						400			
495	cga	atg	gaa	atc	cat	aag	aat	gag	gct	tgg	ctc	tct	gaa	gtc	gaa	ggc	1366
497	Arg	Met	Glu	Ile	His	Lys	Asn	Glu	Ala	Trp	Leu	Ser	Glu	Val	Glu	Gly	
499		405					410						415				
503	aaa	aca	ggt	ggg	aga	gga	gac	aga	aga	cat	agc	agt	gac	ata	aat	cat	1414
505	Lys	Thr	Gly	Gly	Arg	Gly	Asp	Arg	Arg	His	Ser	Ser	Asp	Ile	Asn	His	
507	420					425				430						435	
511	ctt	gta	aca	cag	gga	cga	gaa	agt	cct	gag	gga	agt	tac	act	gat	gat	1462
513	Leu	Val	Thr	Gln	Gly	Arg	Glu	Ser	Pro	Glu	Gly	Ser	Tyr	Thr	Asp	Asp	
515				440						445						450	
519	gca	aac	cag	gaa	gtc	cgt	ggg	cca	ccc	cag	cag	cat	ggt	cac	cac	aat	1510
521	Ala	Asn	Gln	Glu	Val	Arg	Gly	Pro	Pro	Gln	Gln	His	Gly	His	His	Asn	
523				455						460						465	
527	gag	ttt	gat	gat	gaa	ttt	gag	gat	gat	gat	ccc	ttg	cct	gct	att	gga	1558
529	Glu	Phe	Asp	Asp	Glu	Phe	Glu	Asp	Asp	Asp	Pro	Leu	Pro	Ala	Ile	Gly	
531			470					475						480			
535	cac	tgc	aaa	gct	atc	tac	cct	ttt	gat	gga	cat	aat	gaa	ggt	act	cta	1606
537	His	Cys	Lys	Ala	Ile	Tyr	Pro	Phe	Asp	Gly	His	Asn	Glu	Gly	Thr	Leu	
539			485					490						495			
543	gca	atg	aaa	gaa	ggt	gaa	ggt	ctc	tac	att	ata	gag	gag	gac	aaa	ggt	1654
545	Ala	Met	Lys	Glu	Gly	Glu	Val	Leu	Tyr	Ile	Ile	Glu	Glu	Asp	Lys	Gly	
547	500					505				510						515	
551	gac	gga	tgg	aca	aga	gct	cgg	aga	cag	aac	ggt	gaa	gaa	ggc	tac	gtt	1702
553	Asp	Gly	Trp	Thr	Arg	Ala	Arg	Arg	Gln	Asn	Gly	Glu	Glu	Gly	Tyr	Val	
555					520					525						530	

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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 Seq#:7; Xaa Pos. 53
 Seq#:8; Xaa Pos. 53
 Seq#:9; N Pos. 64,65
 Seq#:11; N Pos. 22
 Seq#:15; N Pos. 56,66,83,104,112,113,135
 Seq#:21; N Pos. 1303
 Seq#:29; N Pos. 324
 Seq#:29; Xaa Pos. 5
 Seq#:30; Xaa Pos. 5
 Seq#:45; N Pos. 3082

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 1,3,10,14,17,20,23,26,29,32,34,36,37,38,39,41,42,43,44,46
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 Seq#:1; Line(s) 118,120,122,124,126,128,130,132,134,136,138,140,142,144,146
 Seq#:1; Line(s) 148,150,152,154,156,158,160,163
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